

0590
1/26

#4



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RAW SEQUENCE LISTING

DATE: 12/09/2002 P.6

PATENT APPLICATION: US/10/065,200A

TIME: 13:03:56

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\12092002\J065200A.raw

3 <110> APPLICANT: Wisnewski, Nancy
 4 Becher, Anna M.
 5 Jarvis, Eric
 7 <120> TITLE OF INVENTION: NOVEL FLEA ECDYSONE AND ULTRASPIRACLE NUCLEIC ACID
 MOLECULES, PROTEINS
 8 AND USES THEREOF
 10 <130> FILE REFERENCE: FC-4-1
 12 <140> CURRENT APPLICATION NUMBER: 10/065,200A
 C--> 13 <141> CURRENT FILING DATE: 2002-11-18
 15 <150> PRIOR APPLICATION NUMBER: 09/435,019
 16 <151> PRIOR FILING DATE: 1999-11-05
 18 <150> PRIOR APPLICATION NUMBER: 60/107,559
 19 <151> PRIOR FILING DATE: 1998-11-06
 21 <160> NUMBER OF SEQ ID NOS: 71
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 446
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Ctenocephalides felis
 30 <400> SEQUENCE: 1
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 33 cgaaaggaaa agaaggcaca gaaggaaaag gacatcggac caatatcagg taccgttgga 120
 35 aaatctgctg ctcccttagc gaattctgca ttacttcaga agcctgatat ttgacctgcg 180
 37 gtcatagaat gcgacccatt acctccagaa gcaactaaag tgaaattttt gtcagacaag 240
 39 attcttgctg aaaacagaat tcgaaatggt ccacctttga ctgcaaatca agaatatgtg 300
 41 atcgcaagat tagtggtgta ccaagatgga tatgaacaac cttctgagga agacctacga 360
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 45 attaccatac ttactgtgca gcttat 446
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 50 <212> TYPE: DNA
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 58 tcttggtacc aactaatct tgcgacaca tattcttgat ttgcagtcaa aggtggaaca 180
 60 tttcgaattc tgttttcagc aagaatcttg tctgacaaaa atttcacttt agttgcttct 240
 62 ggaggtaatg ggtcgcatct catgaccgca ggcaaaatat caggcttctg aagtaatgca 300
 64 gaattcgcta agggagcagc agattttcca acggtacctg atattggtcc gatgtccttt 360
 66 tccttctgtg ccttcttttc ctttcgcttc atggcgcatg ggttttcggg aaccacgcac 420
 68 tcggggcgca ttccgacagc caaaca 446
 71 <210> SEQ ID NO: 3
 72 <211> LENGTH: 350
 73 <212> TYPE: DNA

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81 cggtcacatgaa atgcgaccca ttacctccag aagcaactaa agtgaaattt ttgtcagaca      180
83 agattcttgc tgaaaacaga attcgaaatg ttccaccttt gactgcaa at caagaatatg      240
85 tgatcgcaag attagtgtgg taccaagatg gatatgaaca accttctgag gaagacctac      300
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98 ctcagaaggt tgttcataatc catcttggtta ccacactaat cttgcgatca catattcttg      120
100 atttgcagtc aaaggtggaa catttcgaat tctgttttca gcaagaatct tgtctgacaa      180
102 aaatttcact ttagttgctt ctggaggtaa tgggtcgcat ttcattgaccg caggcaaaat      240
104 atcaggcttc tgaaggaatg cagaattcgc taaggaggca gcagattttc caacggtacc      300
106 tgatattgcc gatgtccttt tccttctgtg ccttcttttc ctttcgcttc      350
109 <210> SEQ ID NO: 5
110 <211> LENGTH: 2822
111 <212> TYPE: DNA
112 <213> ORGANISM: Ctenocephalides felis
114 <220> FEATURE:
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116 <222> LOCATION: (605)..(2287)
117 <223> OTHER INFORMATION:
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123 atgtataatt gtatttgtga aatgaaacac atgctacctta aaaactgatt cgtatgccgc      120
125 tctatcaatc agaaatgata attaaacaat ttttttatat tgaaatagaa catattatgt      180
127 tcatatgtca ataacaaatt ttaaaccattc atccaagtta cctattttat gcttttaaga      240
129 tattattttat ttattttattt tgttttgtaa aattttaaaat ttacataaaa tacttttctaa      300
131 ctatgaatat aaattaatat acaaaaagatt ttgaaactaa gaggaaaagt aattataatc      360
133 attttaatca ttaaattata tactcaaaaat gatacaatta gattttacag tcacacacat      420
135 taggtacaga gattcaatta tgaattagga gttgagaaat gctttcgagt aaaatctgca      480
137 ataagatgac tatattccta aggatgttat gtcagtcata aataaaaaatc actatatttt      540
139 caatttgtgt atggtgatct tctaaaggat aaatgtgtga agtgaaatac cttgcattat      600
141 caac atg aaa cga cgt tgg tct aac aac ggt ggc ttc caa acc ttg cgg      649
142 Met Lys Arg Arg Trp Ser Asn Asn Gly Gly Phe Gln Thr Leu Arg
143 1 5 10 15
145 atg ctc gaa gat gtt gca tct ggt gag gta acg tcg tct tct ggt ggc      697
146 Met Leu Glu Asp Val Ala Ser Gly Glu Val Thr Ser Ser Ser Gly Gly
147 20 25 30
149 gcc ctg gct gcg ttg agt ccg gct tcg tta ggt tcg ccc gag aca tat      745
150 Ala Leu Ala Ala Leu Ser Pro Ala Ser Leu Gly Ser Pro Glu Thr Tyr
151 35 40 45
153 gcc gag ctg gat ttg tgg gtg tac gag gaa gct ggc tta cat cca ggt      793
154 Ala Glu Leu Asp Leu Trp Val Tyr Glu Glu Ala Gly Leu His Pro Gly

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155	50	55	60	
157	tca ggt gtg caa gga tgc ggt gcg gtc gcc gcc ttg cca tgc atc gcg	841		
158	Ser Gly Val Gln Gly Cys Gly Ala Val Ala Ala Leu Pro Ser Ile Ala			
159	65 70 75			
161	aca cag gtc ccc cta gga ttg ccc gct atg gac cta ccg cac acg cct	889		
162	Thr Gln Val Pro Leu Gly Leu Pro Ala Met Asp Leu Pro His Thr Pro			
163	80 85 90 95			
165	cgg agt gac agt gcg ggt agc atc tca tca gga cga gaa gac ctg tca	937		
166	Arg Ser Asp Ser Ala Gly Ser Ile Ser Ser Gly Arg Glu Asp Leu Ser			
167	100 105 110			
169	ccg cct agt tct ttg aac ggc tat tca gca gat ggc tgc gaa gcg aag	985		
170	Pro Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asp Gly Cys Glu Ala Lys			
171	115 120 125			
173	aag gcc aag aaa ggg ccg gcg ccg cag cag gag gaa cta tgt ctt	1033		
174	Lys Ala Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu Cys Leu			
175	130 135 140			
177	gtg tgc ggc gac cgt gcc tcc gga tat cat tac aac gct ctt act tgt	1081		
178	Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys			
179	145 150 155			
181	gaa gga tgc aaa ggt ttt ttc cga cga agt gtg act aag aat gcc gtg	1129		
182	Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val			
183	160 165 170 175			
185	tac gtg tgc aag ttt ggg cac acg tgc gaa atg gac atg tat atg cga	1177		
186	Tyr Val Cys Lys Phe Gly His Thr Cys Glu Met Asp Met Tyr Met Arg			
187	180 185 190			
189	cgc aaa tgt cag gaa tgt agg ctc aag aaa tgt ttg gct gtc gga atg	1225		
190	Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met			
191	195 200 205			
193	cgc ccc gag tgc gtg gtt ccc gaa aac caa tgc gcc atg aag cga aag	1273		
194	Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Lys			
195	210 215 220			
197	gaa aag aag gca cag aag gaa aag gac atc gga cca ata tca ggt acc	1321		
198	Glu Lys Lys Ala Gln Lys Glu Lys Asp Ile Gly Pro Ile Ser Gly Thr			
199	225 230 235			
201	gtt gga aaa tct gct gct ccc tta gcg aat tct gca tta ctt cag aag	1369		
202	Val Gly Lys Ser Ala Ala Pro Leu Ala Asn Ser Ala Leu Leu Gln Lys			
203	240 245 250 255			
205	cct gat att ttg cct gcg gtc atg aaa tgc gac cca tta cct cca gaa	1417		
206	Pro Asp Ile Leu Pro Ala Val Met Lys Cys Asp Pro Leu Pro Pro Glu			
207	260 265 270			
209	gca act aaa gtg aaa ttt ttg tca gac aag att ctt gct gaa aac aga	1465		
210	Ala Thr Lys Val Lys Phe Leu Ser Asp Lys Ile Leu Ala Glu Asn Arg			
211	275 280 285			
213	att cga aat gtt cca cct ttg act gca aat caa gaa tat gtg atc gca	1513		
214	Ile Arg Asn Val Pro Pro Leu Thr Ala Asn Gln Glu Tyr Val Ile Ala			
215	290 295 300			
217	aga tta gtg tgg tac caa gat gga tat gaa caa cct tct gag gaa gac	1561		
218	Arg Leu Val Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp			
219	305 310 315			

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221 cta cga agg ata atg ata agt aca cca gct gaa gat gaa gct ctt gaa      1609
222 Leu Arg Arg Ile Met Ile Ser Thr Pro Ala Glu Asp Glu Ala Leu Glu
223 320                               325                               330                               335
225 ttt cgg cat ata act gaa att acc ata ctt act gtg cag ctt ata gtg      1657
226 Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val
227                               340                               345                               350
229 gaa ttt gca aag ggt tta cca gct ttt acc aaa ata cca caa gaa gat      1705
230 Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp
231                               355                               360                               365
233 caa ata aca tta tta aag gca tgt tca agt gaa gta atg atg ctg cga      1753
234 Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg
235                               370                               375                               380
237 atg gct cgg cgg tac gat gca gtg tcg gat tca atc tta ttc gcg aat      1801
238 Met Ala Arg Arg Tyr Asp Ala Val Ser Asp Ser Ile Leu Phe Ala Asn
239                               385                               390                               395
241 aat cgt tca tat act cgt gac tcc tat aaa atg gct ggt atg gca gat      1849
242 Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp
243 400                               405                               410                               415
245 aca ata gaa gat cta ttg cat ttt tgt cga cag atg tat act atg act      1897
246 Thr Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Tyr Thr Met Thr
247                               420                               425                               430
249 gta gac aat gtg gag tat gca cta ata aca gca att gtg att ttt tca      1945
250 Val Asp Asn Val Glu Tyr Ala Leu Ile Thr Ala Ile Val Ile Phe Ser
251                               435                               440                               445
253 gat cga cct gga ttg gaa caa gca gat ctt gtg gaa caa att caa agt      1993
254 Asp Arg Pro Gly Leu Glu Gln Ala Asp Leu Val Glu Gln Ile Gln Ser
255                               450                               455                               460
257 tat tac atc aaa aca tta aag tgc tac att ttg aat cga cat agt ggt      2041
258 Tyr Tyr Ile Lys Thr Leu Lys Cys Tyr Ile Leu Asn Arg His Ser Gly
259                               465                               470                               475
261 gac cct aag tgt gga ata ttg ttt gcc aaa ctt ctt att ctt act      2089
262 Asp Pro Lys Cys Gly Ile Leu Phe Ala Lys Leu Leu Ser Ile Leu Thr
263 480                               485                               490                               495
265 gaa tta cgc acg tta gga aat caa aac tca gaa atg tgt ttt gca ctg      2137
266 Glu Leu Arg Thr Leu Gly Asn Gln Asn Ser Glu Met Cys Phe Ala Leu
267                               500                               505                               510
269 aaa ttg aag aac aga aaa ctt cct aga ttt tta gaa gaa att tgg gat      2185
270 Lys Leu Lys Asn Arg Lys Leu Pro Arg Phe Leu Glu Glu Ile Trp Asp
271                               515                               520                               525
273 gtg aca gat aat gtg cct cct acg ata gac agc atg cat agt gta tcg      2233
274 Val Thr Asp Asn Val Pro Pro Thr Ile Asp Ser Met His Ser Val Ser
275                               530                               535                               540
277 gag aat ttc tat aat aat gaa agt aat ggt acc agt gat tct aca cca      2281
278 Glu Asn Phe Tyr Asn Asn Glu Ser Asn Gly Thr Ser Asp Ser Thr Pro
279                               545                               550                               555
281 atg taa agtgctcaga aaatcaacag ctcttttgca tatttgttta ctgtgtactg      2337
282 Met
283 560
285 gtatggaaaa ttaaggtaac attaaaaatat tacataagca ccatgggaaa aggccgttaa      2397

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287 ggcaatatattt ttgaataaat aatctattga gacggtacca atggtaaact tggaaaaaat 2457
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291 tgcttgtgta acacttcaat ggccttcaat aaaataatgt ttaacaacgt cgataggaaa 2577
293 ttaaaaagaa atcatgtgta ataaaatcat ttgtaggccg gccatactga tttacctata 2637
295 ttaagcagaa acttcttaat gtataaatat atttttgctt tgcaaggtaa aaccttctca 2697
297 atgcaacaat gaattatata tataaacatt gattatttta tcgttagaat ttgaattttg 2757
299 tgttgtggga gaattgtatt tggattagat aaataggctg tgaaaaataa aaaaaaaaaa 2817
301 aaaaaa 2822
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305 <211> LENGTH: 560
306 <212> TYPE: PRT
307 <213> ORGANISM: Ctenocephalides felis
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316 20 25 30
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320 35 40 45
323 Glu Leu Asp Leu Trp Val Tyr Glu Glu Ala Gly Leu His Pro Gly Ser
324 50 55 60
327 Gly Val Gln Gly Cys Gly Ala Val Ala Ala Leu Pro Ser Ile Ala Thr
328 65 70 75 80
331 Gln Val Pro Leu Gly Leu Pro Ala Met Asp Leu Pro His Thr Pro Arg
332 85 90 95
335 Ser Asp Ser Ala Gly Ser Ile Ser Ser Gly Arg Glu Asp Leu Ser Pro
336 100 105 110
339 Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asp Gly Cys Glu Ala Lys Lys
340 115 120 125
343 Ala Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu Cys Leu Val
344 130 135 140
347 Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu
348 145 150 155 160
351 Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr
352 165 170 175
355 Val Cys Lys Phe Gly His Thr Cys Glu Met Asp Met Tyr Met Arg Arg
356 180 185 190
359 Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg
360 195 200 205
363 Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Lys Glu
364 210 215 220
367 Lys Lys Ala Gln Lys Glu Lys Asp Ile Gly Pro Ile Ser Gly Thr Val
368 225 230 235 240
371 Gly Lys Ser Ala Ala Pro Leu Ala Asn Ser Ala Leu Leu Gln Lys Pro
372 245 250 255
375 Asp Ile Leu Pro Ala Val Met Lys Cys Asp Pro Leu Pro Pro Glu Ala
376 260 265 270
379 Thr Lys Val Lys Phe Leu Ser Asp Lys Ile Leu Ala Glu Asn Arg Ile
380 275 280 285

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; N Pos. 15

Seq#:51; N Pos. 10

VERIFICATION SUMMARY

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L:120 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:117
L:565 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:562
L:990 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:987
L:1527 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:1524
L:2229 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:2226
L:2556 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:2553
L:2853 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:2850
L:3206 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:35,Line#:3203
L:3739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
L:3817 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0